

1. 2. 3.

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3 Sequences Aligned      Alignment Score = 989
Gaps Inserted = 3        Conserved Identities = 35

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Multiple Alignment Parameters:
 Open Gap Penalty = 5.0 Extend Gap Penalty = 0.0
 Delay Divergent = 40% Gap Distance = 8
 Similarity Matrix: blosum

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hu_Secs-1      1  MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVPSPNST  50
mu_Secs-1      1  MRLALSGLLCMLLLCFCIFSSEGRRHPAKSLKLRR---CCHLSPRSKLT  47
ra_Secs-1      1  MRLTLTSLGLFFMLFLCLCVLSSEGRKRPAPKFKLP---RCHLSPRSKPI  47
          **** * * * * * * * * * * * * * * * * *

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hu_Secs-1  51 NLKGHHVRLCKPCKLEPEPRLWVVP GALPQV  81
mu_Secs-1  48 TWKGNHTRPCRLCRNKL PVKSWVVP GALPQI  78
ra_Secs-1  48 TWKGNHTRPCRPCR-KLESNSWVVP GALPQI  77
          * * * * * * * * * *

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APPENDIX B

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SEQ ID NO:4 vs. AA422178

	10	20	30	40	50	60
SEQ ID NO:4	GGAACGAGGG	AAAATCTGCC	TTCTCACCAT	GAGGCTTCTA	GTCCTTTCCA	GCCTGCTCTG
AA422178		ATCTGCC	TTCTCACCAT	GAGGCTTCTA	GTCCTTTCCA	GCCTGCTCTG

	70	80	90	100	110	120
SEQ ID NO:4	TATCCTGCTT	CTCTGCTTCT	CCATCTTCTC	CACAGAGGG	AAGAGGCGTC	CTGCCAAGGC
AA422178	TATCCTGCTT	CTCTGCTTCT	CCATCTTCTC	CACAGAGGG	AAGAGGCGTC	CTGCCAAGGC

	130	140	150	160	170	180
SEQ ID NO:4	CTGGTCAGGC	AGGAGAACCA	GGCTCTGCTG	CCACCGAGTC	CCTAGCCCCA	ACTCAACAAA
AA422178	CTGGTCAGGC	AGGAGAACCA	GGCTCTGCTG	CCACCGAGTC	CCTAGCCCCA	ACTCAACAAA

	190	200	210	220	230	240
SEQ ID NO:4	CCTGAAAGGA	CATCATGTGA	GGCTCTGTAA	ACCATGCAAG	CTTGAGCCAG	AGCCCCGCCT
AA422178	CCTGAAAGGA	CATCATGTGA	GGCTCTGTAA	ACCATGCAAG	CTTGAGCCAG	AGCCCCGCCT

	250	260	270	280	290	300
SEQ ID NO:4	TTGGGTGGTG	CCTGGGGCAC	TCCCACAGGT	GTAGCACTCC	CAAAGCAAGA	CTCCAGACAG
AA422178	TTGGGTGGTG	CCTGGGGAG	TCCCACAGGT	GTAGCACTCC	CAAAGCAAGA	CTCCAGACAG

	310	320	330	340	350	360
SEQ ID NO:4	CGGAGAACCT	CATGCCTGGC	ACCTGAGGTA	CCCAGCAGCC	TCCTGTCTCC	CCTTTCAGCC
AA422178	CGGAGAACCT	CATGCCTGGC	ACCTGAGGTA	CCCAGCAGCC	TCCTGTCTCC	CCTTTCAGCC

	370	380	390	400	410	420
SEQ ID NO:4	TTCACAGCAG	TGAGCTGCAA	TGTTGGAGGG	CTTCATCTCG	GGCTGCAAGG	ACCCTGGGAA
AA422178	TTCACAGCAG	TGAGCTGCAA	TGTTGGAGGG	CTTCATCTCG	GGCTGCAAGG	ACCCTGGGAA

	430	440	450	460	470	480
SEQ ID NO:4	AGTTCAGAA	CTCCACGTCC	TTGTCTCAAT	TGTGCCATCA	ACTTTCAGAG	CTATCATGAG
AA422178	AGTTCAGAA	CTCCACGTCC	TTGTCTCAAT	TGTGCCATCA	ACTTTCAGAG	CTATCATGAG>

	490	500	510	520	530	540
SEQ ID NO:4	CCAACCTCAC	CCCACAGGGC	CTCAGTCGCC	ACCATGTGGG	CCTCTCCAGT	GCAACCACC
AA422178	CCAACCTCAC	CCCACAGGGC	CTCAGTCGCC	ACCATGT		

	550	560	570	580	590	600
SEQ ID NO:4	GAGCATTCCA	CCATGACCGG	TCACAGCTAC	AAATCCAGAG	ACCATCAATC	CTGCTAGAGT
	610	620	630	640	650	660
SEQ ID NO:4	GCAGGGTGGC	AAGCACCCAA	GGGTGGCTGA	CCAAGACTGC	AGAGTCTCCT	CCATCTTCAG
	670	680	690	700	710	720
SEQ ID NO:4	GTCCATTTCAG	CCTCCTGGCA	TTTAACTACC	AGCATCCAGT	GGTCCCCAAG	GAATCCCTTC
	730	740	750	760	770	780
SEQ ID NO:4	CTAGCCTCCT	GACATGAGTC	TGCTGGAAAG	AGCATCCAAA	CAAACAAGTA	ATAAATAAAT
	790	800				
SEQ ID NO:4	AAATAAACTC	AATGCAGACA	CAAAAA			